

REMARKS

Claim Status

Claims 1-19 are pending in the application. Claims 9-19 are canceled with this amendment as directed to non elected subject matter. By this amendment, claims 1 and 8 are amended, new claims 20-23 are added, and claims 2-7 are canceled. Claims 1 and 8 have been amended to combine the subject matter of former claim 1 or 8, respectively, with the subject matter of claims 2 to 7. Applicants respectfully submit that the amendments to the claims do not introduce any new subject matter into the application.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 4, 6, and 8 are rejected under 35 U.S.C. § 112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Applicant respectfully disagree, nevertheless in order to advance the case to allowance, claims 4 and 6 have been deleted and claim 8 (and claim 1) has been amended to include the limitations of claims 4 and 6.

Claims 1 and 8 are amended to recite that the assay is directed to the identification of bacteria using as markers the Spy0160 sequences (i.e., SEQ ID NOS: 1-62, and 326-359) and the Ecs0036 sequences (SEQ ID NOS: 194-232, 238-239, 242-254, and 431-442). Spy0161 and Ecs0036 were elected in the Response to the election of species requirement of June 11, 2009.

In further response to the rejection, "Spy0161" refers to an open reading from (Accession no. AE006485.1, position 3201 to 4030) homologous for the gene purA. Conserved sequences similar to Spy0160 are present in almost all Gram-positive bacteria. See present specification at page 21, line 4 to page 22, line 5.

The same is true for "Ecs0036" (Accession No. AP002550, position 35200-36200) which corresponds to the gene carB. Conserved sequences for Ecs0036 are present in almost all Gram-negative bacteria. See present specification at page 24, lines 8-14.

The claims now recite the SEQ ID NOS that correspond to the elected species. The Examiner is referred to Table 1 on pages 5-6 of the specification as filed which shows the correlation between the Spy0161 & Ecs0036, their respective genes, PurA and carB, and the

homologous sequences corresponding to the genes. The specification teaches that these are markers for Gram-positive and Gram-negative bacteria respectively.

Claim 8 has been amended to include a “diagnosing” step.

In view of Applicants’ amendments and Remarks, reconsideration and withdrawal of the above ground of rejection is respectfully requested.

Rejection under 35 U.S.C. § 112, first paragraph – written description

Claims 1-4, 6, and 8 are rejected under 35 U.S.C. § 112, first paragraph as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s) had possession of the claimed invention at the time that the application was filed.

Applicant respectfully disagree, nevertheless in order to advance the case to allowance, claims 1 and 8 have been amended to specify the SEQ ID NOs 1-62, 326-359 listed in claim 5 and SEQ ID NOs 194-232, 238-239, 242-254, and 431-442 listed in claim 7. As discussed above, these sequences correspond to the homologs associated with Spy0160 and Ecs0036. Claim 1 has been amended to limit the scope to “bacteria”. Claim 8 is already limited to “bacterial infections”.

Accordingly, the claims now recite sequences for which a specific structure is provided in the specification. The sequences recited in the claims clearly have written description support. As the structures of the homolog sequences are provided, one skilled in the art would know how to design probes or primers by chemical synthesis to detect PurA and carB.

As explained above, the recited sequences belong to two families as indicated by Table 1 on pages 5 and 6 and as discussed above. The recited sequences SEQ ID NOs 1-62 and 326-359 relate to detection of the PurA gene, marker I for Gram-positive bacteria. The specification teaches that these sequences are conserved in Gram-positive bacteria (specification as filed, page 9, lines 33-35; also Figure 1). The recited SEQ ID NOS: 194-232, 238-239, 242-254, and 431-442 relate to detection of carB, marker V for Gram-negative bacteria. The specification teaches that these sequences are conserved in Gram-negative bacteria (specification as filed, page 10, lines 4-6; also Figure 8).

With regards to Spy0160 (PurA, Marker 1), this marker is described in the specification, particularly at page 21, line 4 to page 22, line 5. Example 3, Table 3A describes use of Spy0160 homologs as a target. Furthermore, the specification (page 22, last paragraph) teaches :

A further analysis has been performed on reference strains and on several hundreds clinical strains provided by Belgian hospitals. The conservation of targets of interest (purA and ptsI (i.e. Marker I and II) has been confirmed in the genome of all these reference and clinical strains. This analysis confirmed the very little genomic variability of these sequences within a species of interest. This feature is crucial to allow the use of these marker sequences in a strategy of multigenotypic identification of Gram-positive bacteria.

Accordingly, Marker 1 Spy0160, has been shown to be present in “several hundreds of strains”.

Ecs0036 is defined in the present specification at page 24, lines 8-14. Example 3, Table 3F describes use of Ecs0036 homologs as target.

Markers I (Spy0176) and V (Ecs0036), according to the claimed invention, are illustrated in Figures 1 and 8, for a range of Gram-positive and Gram-negative, resp., bacterial strains. The use of Marker 1 (Spy0176) for identification of *Bacillus* species is exemplified in Example 4, Table 4.

By reliance upon two highly conserved marker genes, one for Gram-positive and one for Gram-negative, the combined result provides a method by which the presence of Gram-positive or Gram-negative bacteria may be determined. The homologs for the two elected species (Spy0160 & Ecs0036) are recited in the claims. These homologs are described by the sequences associated with their SEQ ID NOS. The specification teaches the conservation of these homologs and their specificity for Gram-positive and Gram-negative bacteria. The presence of these homologs in a number of Gram-positive and Gram-negative bacteria is exemplified. The use of these markers to determine the presence of bacteria is described and exemplified. Accordingly, Applicants believe that the present claims meet the written description requirement of 35 U.S.C. § 112, first paragraph.

By the practice of the claimed method, the gram-phenotype of bacteria in a sample can be rapidly determined. This allows for an effective antibiotic therapy to be prescribed quickly for the patient.

In view of Applicants' amendments and arguments, reconsideration and withdrawal of the above ground of rejection is respectfully requested.

Claims rejection under 35 USC § 112 first paragraph – Enablement

Claims 1-4, 6 and 8 are rejected under 35 USC § 112 first paragraph, because the specification while being enabling for (i) methods for detecting *Bacillus anthracis* Sterne comprising obtaining a nucleic acid sample, analyzing the nucleic acid sample for the presence or absence of nucleic acids comprising SEQ ID NO: 14 and detecting the presence of nucleic acids comprising SEQ ID NO: 14 as indicative of the presence of *Bacillus anthracis* Sterne; and (ii) method for detecting *Francisella tularensis* comprising obtaining a nucleic acid sample, analyzing the nucleic acid sample for the presence or absence of nucleic acids comprising SEQ ID NO: 230 and detecting the presence of nucleic acids comprising SEQ ID NO: 230 as indicative of the presence of *Francisella tularensis*, does not reasonably provide enablement for the method as claimed.

Applicant respectfully disagree, nevertheless in order to advance the case to allowance, claims 1 and 8 have been amended as discussed above. For the reasons provided above in response to the rejection based upon inadequate written description, Applicant respectfully submits that the amended claims are enabled.

Additionally, two new independent claims (20 and 22) are presented which are directed to the subject matter which the Examiner considers as enabled.

Furthermore, Applicants present new claim 21, directed to the detection of *Staphylococcus aureus* for which support is found in Example 5 and new claim 23, directed to the detection of *Brucella*, which finds support in Examples 2 and 3 and Figure 9.

As new claims 20-23 correspond to exemplified species, Applicants' respectfully submit that these claims, at least, are enabled.

In view of Applicants' amendments and arguments, reconsideration and withdrawal of the above ground of rejection is respectfully requested.

Rejection under 35 U.S.C. § 102(b)

Claims 1-3 and 8 are rejected under 35 U.S.C. § 102(b) as being anticipated by Klaschik, et al. (Journal of Clinical Microbiology, November 2002, 40: 4304-4307, IDS).

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Applicants respectfully disagree nevertheless in order to advance the case to allowance, the subject matter of claims 1 and 8 was amended.

The present claims are not anticipated by Klaschik et al., since this document is completely silent on an assay for detecting and identifying one or more bacteria in a sample using at least one molecular marker conserved in Gram-positive bacteria and selected from the group comprising the sequences with SEQ ID NOs 1-62, 326-359, and at least one molecular marker conserved in Gram-negative bacteria and selected from the group comprising the sequences with SEQ ID NOs 194-232, 238-239, 242-254, and 431-442.

In view of Applicants' amendments and remarks, withdrawal of the rejection is respectfully requested.

No Disclaimers or Disavowals

Although the present communication may include alterations to the application or claims, or characterizations of claim scope or referenced art, Applicant is not conceding in this application that previously pending claims are not patentable over the cited references. Rather, any alterations or characterizations are being made to facilitate expeditious prosecution of this application. Applicant reserves the right to pursue at a later date any previously pending or other broader or narrower claims that capture any subject matter supported by the present disclosure, including subject matter found to be specifically disclaimed herein or by any prior prosecution. Accordingly, reviewers of this or any parent, child or related prosecution history shall not reasonably infer that Applicant has made any disclaimers or disavowals of any subject matter supported by the present application.

CONCLUSION

In view of Applicants' amendments to the claims and the foregoing Remarks, it is respectfully submitted that the present application is in condition for allowance. Should the Examiner have any remaining concerns which might prevent the prompt allowance of the application, the Examiner is respectfully invited to contact the undersigned at the telephone number appearing below.

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Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

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By: Che Cherskin
Che Swyden Cherskin, Ph.D.
Registration No. 41,466
Agent of Record
Customer No. 20,995
(949) 721-6385

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012110